

Supplementary Table 1. Initiation region sequences for Figures 1, 2, and 3.

Name	Sequence
Rad23 L1	PRSTKTKVTEPIAPESATTPGRENSTEASPSTDASAAPAATAPEGSQPQEEQTATT ERTESASTPGFVVGT
Rad23 L2	PRGI PENLRQPEPQQQTAAAAEQPSTAATTAEQPAEDDLFAQAAQGGNASSGALGTT GGATDAAQGG
Rad23 L3	PRANPEVFVSMILLEAVGDNMQDVMEGADDMVEGEDIEVTGEAAAAGLGQGEGEGSFQ VDYTP
64	PRLRYQPLLRIQNCEAAILRASQTRLNTIGAYGSTVPRSQSFEQDSRQRSGRISPA EHHHHHH
102	PRLRYQPLLRIQNCEAAILRASQTRLNTIGAYGSTVPRSQSFEQDSRQRTQSWTAL RVGAIPAATSSVAYLNWHNGQIDNEPQLDMNRQRISPAEHHHHHH
15	PRGRISPSPAEEHHHHHH
Acidic tail	PRDDDENGSVILQDDDYDDGNNHIPFEDDDVYNYNNDNDDEERIEFEDDDDDDSI DNDSVMDRKQPHKAEDEDSEVEDVERVSKKI
95	PRMLRYQPLLRIQNCEAAILRASQTRLNTIGAYGSTVPRSQSFEQDSRQRTQSWTA LRVGAIPAATSSVAYLNWHNGQIDNEPQLDMNRQRISPAE
39	PRGGGAWLLPVSLVRRRTTLAPNTQTASPRALADSLMQ
NRR	PRRSNCNNNNNDNDKNNGSNCNNNNNDNDKNNGSNCNNNNNDNDKNNGSNCNN NNNDNDKNNGSGT
SRR	PRRSSSTSSDGSSSSSASSSSGSSSTSSDGSSSSSASSSSGSSSTSSDGSSS SSSASSSSGSSSTSSDGSSSSSASSSSGSGTMKHGT

Supplementary Table 2. Initiation regions sequences for Figure 5

Name	Sequence	
SRR	SSSTSSDSGSSSSASSSSGTSSSTSSDSGSSSSSSASSSSGTSSSTSSDSGSSSSSSASSSS	Four copies of residues 178-196 of ICP4
NRR [#]	NCNNNNNDNDKNNGSNCNNNNNDNDKNNNCNNGSNCNNNNNDNDKNNGSNCNNNNNDNDKNN	Four copies of residues 373-386 of SPT23
GRR	EIKDKEEVQRKRQKLMPNFSDSF GGGSGAGAGGGGMFGSGGGG GGTGSTGPGYSFPH	Residues 352-408 of p105
PEST	LQMLPESEDEE SYDTESEFTE FTEDEL PYDDGSL QMLPESEDE ESYDTESEFTE FTEDEL PYDD	Two copies of residues 277-307 of IkB α
RPB	R SYSPTSPNYSPTSPGSYSPTSPNYSPTSPGGSRSYSPTSPNYSPTSPGSYSPTSPNYSPTSPG	Four copies of residues 1688-1702 of RPB1
SP1	SLLTEVETP GSSL LTEVETPGSSL TEVETPGSSL LTEVETPG SSSLTEVETP	Five copies of residue 2-10 of Influenza A virus M2 protein
SP2	PESMREEYRKE GPESMREEYRKEGPESMREEYRKEGPESM REEYRKEGS PESMREEYRKE	Five copies of residue 69-79 of Influenza A virus M2 protein
SP mix	PESMREEYRKEGSSL LTEVETPGSPESMREEYRKEGSSL TEVETPGSPESMREEYRKE ETPGSPESMREEYRKE	Tandem repeat of SP1 and SP2 (SP2-SP1-SP2-SP1-SP2)
NB	KRIKCPDCEPFCNKRGSKRIKCPDCEPFCNKRGSKRIKCPDCE PFCNKRGS	Three copies of residue 58-72 of Influenza B virus Glycoprotein NB
NS2	LIEEVVRHRLKT TENSGSLIEEV RHRLKT TENSGSLIEEV RHRL KT TENSGS	Three copies of residue 79-93 of Influenza A virus NS protein
SNS	PESMREEYRKEGSKRIKCPDCEPFCNKRGSPESMREEYRKE	Tandem repeat of SP2 and NB (SP2-NB-SP2)-
DRR	IDDENGSVILQDDDYDDGNHHIPFEDDDVYNYN DNDDDDERIE FEDDDDDDDDSIDNDSVMDRKQPHKAED EDSEDVEDVERVSKKD	Residue 210-295 of Cdc34
eRR	GGGA WLLPVSLVRRRT LAPNTQTASPRALADSLMQR	Residues 321-354 of lacI
ODC	FPPEVEEQDDGTLPMSCAQESGMDRHPAACASARINV	Residue 106-142 of ornithine decarboxylase
SP231 [#]	SLLTEVETPIRNEWGCRCNDSSD	Residue 2-24 of Influenza A virus M2 protein
Subunit9	MASTRVLASRLASQMAASAKVARPAVRVAQVSKRTIQTGSPLQTRAYSS	Residue 1-44 of ATP synthase protein 9 mitochondrial precursor
35 Δ K	LRYQPLLRI SQNCEAAILRASQTRLNT ISGRISP AEEHHHHHH	Residue 2-29 and 90-95 of yeast cytochrome b_2

*Peptides used for the peptide proteolysis assay (Supplementary Figure 3) are highlighted in red color

Supplementary Table 3. Median half-life of mouse proteins.

Mouse protein half-life data were not normally distributed, statistical significance of the difference in the distributions of half-life values among different classes of proteins was estimated using the non-parametric Wilcoxon rank sum test. Therefore, the difference between any two classes is provided as differences in their median half-lives and not in their average half-lives. The median half-life of all the proteins ($n=4495$) is 48.2 h. The following table provides a comparison of the median half-lives for each class of proteins:

Class	No. of proteins	Median ± C.I. (Half-life in hours)
All proteins	4502	48.2 ± 1.5
<i>N-terminal disordered segments (NDS)</i>		
Proteins without NDS	3785	49.6 ± 1.7
Proteins with NDS without amino acid bias	483	40.7 ± 3.5
Proteins with NDS with amino acid bias	234	48.8 ± 4.9
<i>C-terminal disordered segments (CDS)</i>		
Proteins without CDS	3878	48.8 ± 1.7
Proteins with CDS without amino acid bias	377	41.2 ± 3.7
Proteins with CDS with amino acid bias	247	54.6 ± 5.6

Confidence interval (C.I.) = $1.58(IQR/\sqrt{n})$ (where IQR is the interquartile range and 'n' the number of proteins in each class). Data at the basis of the table are from Schwahnässer, B. *et al.* Global quantification of mammalian gene expression control. *Nature* **473**, 337-342 (2011).

Thus, the median half-lives of proteins with disordered segments and amino acid bias are comparable or slightly higher to the median half-life of all proteins, whereas proteins with disordered segments without amino acid bias have a median half-life shorter by about 8-13 hours. This corresponds to about 17-28% of the median half-life of the analyzed proteins. Such differences in half-lives are relevant in the context of the cell division time and the changes in the proteome content over time.